

0260

OIPE

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/351,149

DATE: 07/28/1999
TIME: 15:00:19

Input Set: I351149.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: THORPE, PHILIP E.
2   RAN, SOPHIA
3 <120> TITLE OF INVENTION: CANCER TREATMENT KITS COMPRISING THERAPEUTIC CONJUGATES
4   THAT BIND TO AMINOPHOSPHOLIPIDS
5 <130> FILE REFERENCE: 4001.002383
6 <140> CURRENT APPLICATION NUMBER: US/09/351,149
7 <141> CURRENT FILING DATE: 1999-07-12
8 <160> NUMBER OF SEQ ID NOS: 5
9 <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 2149
12 <212> TYPE: DNA
13 <213> ORGANISM: Homo sapiens
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17   aaaattttta aatttttagaa caaagctaac aaatggctag ttttctatga ttcttcttca 180
18   aacgctttct ttgaggggga aagagtcaaa caaacaagca gttttacctg aaataaagaa 240
19   ctagtttttag aggtcagaag aaaggagcaa gttttgcgag aggcacggaa ggagtgtgct 300
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21   ggggtgcagca atcagcgccg aagtccagaa aacagtggga gaagatataa cccgattcaa 420
22   catgggcaat gtgcctacac tttcattctt ccagaacacg atggcaactg tcgtgagagt 480
23   acgacagacc agtacaacac aaacgctctg cagagagatg ctccacacgt ggaaccggat 540
24   ttctcttccc agaaacttca acatctggaa catgtgatgg aaaattatac tcagtggctg 600
25   caaaaacttg agaattacat tgtggaaaac atgaagtcgg agatggccca gatacagcag 660
26   aatgcagttc agaaccacac ggctaccatg ctggagatag gaaccagcct cctctctcag 720
27   actgcagagc agaccagaaa gctgacagat gttgagaccc aggtactaaa tcaaacttct 780
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30   atcttagaaa tggaaggaaa acacaaggaa gagttggaca ccttaaagga agagaaagag 960
31   aaccttcaag gcttggttac tcgtcaaaca tatataatcc aggagctgga aaagcaatta 1020
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48      acaagagtct ctacttgggg tgacagtgtc cacgtggctc gactatagaa aactccactg 2040
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52 <211> LENGTH: 498

53 <212> TYPE: PRT

54 <213> ORGANISM: Homo sapiens

55 <400> SEQUENCE: 2

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59      20              25              30
60      Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
61      35              40              45
62      Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
63      50              55              60
64      Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
65      65              70              75              80
66      Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
67      85              90              95
68      Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
69      100             105             110
70      Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
71      115             120             125
72      Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
73      130             135             140
74      Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
75      145             150             155             160
76      Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
77      165             170             175
78      Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
79      180             185             190
80      Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
81      195             200             205
82      Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
83      210             215             220
84      Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
85      225             230             235             240
86      Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
87      245             250             255
88      Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
89      260             265             270
90      Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
91      275             280             285
92      Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
93      290             295             300
94      Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn

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98      Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
99              340              345              350
100     Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
101              355              360              365
102     Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
103              370              375              380
104     Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
105              385              390              395              400
106     Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
107              405              410              415
108     Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
109              420              425              430
110     Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
111              435              440              445
112     Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
113              450              455              460
114     Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
115              465              470              475              480
116     Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
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126     agcaggactg ttcttccac tgcaatctga cagtttactg catgcctgga gagaacacag 180
127     cagtaaaaac caggtttgct actggaaaaa gaggaagag aagactttca ttgacggacc 240
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129     gtgtttgccc tcaagtttgc taagctgctg gtttattact gaagaaagaa tgtggcagat 360
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132     tttcctcctg ccagagatgg acaactgccg ctcttcctcc agcccctacg tgtccaatgc 540
133     tgtgcagagg gacgcgccgc tcgaatacga tgactcgggtg cagaggctgc aagtgttgga 600
134     gaacatcatg gaaaacaaca ctcagtggct aatgaagctt gagaattata tccaggacaa 660
135     catgaagaaa gaaatggtag agatacagca gaatgcagta cagaaccaga cggctgtgat 720
136     gatagaaata gggacaaacc tgttgaacca aacagctgag caaacgcgga agttaactga 780
137     tgtggaagcc caagtattaa atcagaccac gagacttgaa cttcagctct tggaaactc 840
138     cctctcgaca aacaaattgg aaaaacagat tttggaccag accagtgaaa taaacaaatt 900
139     gcaagataag aacagtttcc tagaaaagaa ggtgctagct atggaagaca agcacatcat 960
140     ccaactacag tcaataaaag aagagaaaaga tcagctacag gtgttagtat ccaagcaaaa 1020
141     ttccatcatt gaagaactag aaaaaaaaaat agtgactgcc acggtgaata attcagttct 1080
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153   gaacacaaat aagttcaacg gcattaaatg gtactactgg aaaggctcag gctattcgct 1800
154   caaggccaca accatgatga tccgaccagc agattttctaa acatcccagt ccacctgagg 1860
155   aactgtctcg aactattttc aaagacttaa gcccagtgca ctgaaagtca cggctgcgca 1920
156   ctgtgtcctc ttccaccaca gagggcgtgt gctcgggtgt gacgggacct acatgctcca 1980
157   gattagagcc tgtaaacttt atcacttaaa cttgcatcac ttaacggacc aaagcaagac 2040
158   cctaaacatc cataattgtg attagacaga acacctatgc aaagatgaac ccgaggctga 2100
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<210> SEQ ID NO 4

<211> LENGTH: 496

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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170             20             25             30
171   Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
172             35             40             45
173   Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
174             50             55             60
175   Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
176             65             70             75             80
177   Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
178             85             90             95
179   Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
180             100            105            110
181   Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
182             115            120            125
183   Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
184             130            135            140
185   Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
186             145            150            155            160
187   Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
188             165            170            175
189   Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
190             180            185            190
191   Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
192             195            200            205
193   Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
194             210            215            220

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198                      245                      250                      255
199      Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr
200                      260                      265                      270
201      Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
202                      275                      280                      285
203      Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn
204                      290                      295                      300
205      Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly
206      305                      310                      315                      320
207      Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln
208                      325                      330                      335
209      Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu
210                      340                      345                      350
211      Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg
212                      355                      360                      365
213      Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr
214                      370                      375                      380
215      Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg
216      385                      390                      395                      400
217      Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile
218                      405                      410                      415
219      Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys
220                      420                      425                      430
221      Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp
222                      435                      440                      445
223      Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln
224                      450                      455                      460
225      Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser
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237                      20                      25                      30
238      Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
239                      35                      40                      45
240      Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
241                      50                      55                      60
242      Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Phe Ser Ser Gln Lys Leu
243      65                      70                      75                      80
244      Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp Leu Gln Lys

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